In the Specification:

On page 1, please amend the "Related Applications" paragraph as follows:

This application is a divisional application of U.S. Application Serial No. 09/973,457, filed October 9, 2001, which ~~This application~~ claims priority to U.S. ~~provisional application~~ Provisional Application Serial No. ~~number~~ 60/238,849 filed on October 6, 2000, both of which are hereby ~~the contents of which are~~ incorporated herein by reference in their entirety.

On page 2, please amend the paragraph beginning at line 16 as follows:

Accordingly, in one aspect, the invention features a nucleic acid molecule which encodes a 47174 protein or polypeptide, e.g., a biologically active portion of a 47174 protein. In a preferred embodiment the isolated nucleic acid molecule encodes a polypeptide having the amino acid sequence of SEQ ID NO:2. In other embodiments, the invention provides isolated 47174 nucleic acid molecules having the nucleotide sequence shown in SEQ ID NO:1[[,]] or SEQ ID NO:3 ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number ____~~. In still other embodiments, the invention provides nucleic acid molecules that are substantially identical (e.g., naturally occurring allelic variants) to the nucleotide sequence shown in SEQ ID NO:1[[,]] or SEQ ID NO:3 ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number ____~~. In other embodiments, the invention provides a nucleic acid molecule which hybridizes under a stringent hybridization condition described herein to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1[[,]] or SEQ ID NO:3 ~~or the sequence of the DNA insert of the plasmid deposited with ATCC Accession Number ____~~, wherein the nucleic acid encodes a full length 47174 protein or an active fragment thereof.

On page 10, please amend the paragraph beginning at line 19 as follows:

For general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997) *Protein* 28:405-420 and [[http://]]www.psc.edu/general/ software/packages/pfam/pfam.html.

On page 10, please amend the paragraph beginning at line 22 as follows:

~~A plasmid containing the nucleotide sequence encoding human 47174 (clone "Fbh47174FL") was deposited with American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, VA 20110-2209, on _____ and assigned Accession Number _____. This deposit will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. This deposit was made merely as a convenience for those of skill in the art and is not an admission that a deposit is required under 35 U.S.C. §112.~~

On page 12, please amend the paragraph beginning at line 20 as follows:

As used herein, the term "glycosyltransferase domain" includes an amino acid sequence of about 100-250 amino acid residues in length and having a bit score for the alignment of the sequence to the glycosyltransferase domain (HMM) of at least 30. Preferably, a glycosyltransferase domain includes at least about 120-220 amino acids, more preferably about 120-200 amino acid residues, or about 130-180 amino acids and has a bit score for the alignment of the sequence to the glycosyltransferase domain (HMM) of at least 50 or greater. Glycosyltransferase domains (HMM) have been assigned numerous PFAM Accession Numbers, including PF00534 (group 1) and PF00535 (group 2) ([[http://]]pfam.wustl.edu/). An alignment of the glycosyltransferase domain (amino acids 154 to 336 of SEQ ID NO:2) of human 47174 with a consensus amino acid sequence (group 2 glycosyltransferases) derived from a hidden Markov model is depicted in Figure 2.

On page 23, please amend the paragraph beginning at line 14 as follows:

The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch ((1970) *J Mol Biol* (48):444-453) algorithm which has been incorporated into the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at [[http://]]www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred

set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.